

ATGAGAAGGTGTAGAATAAGTGGGAGGCCCGGCGCCCCCGGTGTCCCCGCCAGGCC
MetArgArgCysArgIleSerGlyArgProProAlaProProGlyValProAlaGlnAla

CCTGTCTCCCAGCCTGATGCCCTGGCCACCAGAGGAAGTGGTGTCAAGGATAGATGTG
ProValSerGlnProAspAlaProGlyHisGlnArgLysValValSerTrpIleAspVal

TATACTCGCGCTACCTGCCAGCCCCGGAGGTGGTGGTGCCTTGACTGTGGAGCTCATG
TyrThrArgAlaThrCysGlnProArgGluValValValProLeuThrValGluLeuMet

GGCACCGTGGCAAACAGCTGGTGCCTGGAGCTGCGTGACTGTGCAGCGCTGTGGTGGCTGC
GlyThrValAlaLysGlnLeuValProSerCysValThrValGlnArgCysGlyGlyCys

TGCCCTGACGATGGCCTGGAGTGTGCCCAGGGCAGCACCAAGTCCGGATGCAGATC
CysProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMetGlnIle

CTCATGATCCGGTACCCGAGCAGTCAGCTGGGGAGATGTCCCTGGAAGAACACAGCCAG
LeuMetIleArgTyrProSerSerGlnLeuGlyGluMetSerLeuGluGluHisSerGln

TGTGAATGCAGACCTAAAAAAAGGACAGTGCCTGTGAAGCCAGACAGGGCTGCTACTCCC
CysGluCysArgProLysLysAspSerAlaValLysProAspArgAlaAlaThrPro

CACCAACCGTCCCCAGCCCCGTTCTGTTCCGGGCTGGGACTCTGCCCGGAGCACCCCTCC
HisHisArgProGlnProArgSerValProGlyTrpAspSerAlaProGlyAlaProSer

CCAGCTGACATCACCAATCCCACTCCAGCCCCAGGCCCTCTGCCAACGCTGCACCCAG
ProAlaAspIleThrGlnSerHisSerProArgProLeuCysProArgCysThrGln

CACCAACCAAGTCCCTGACCCCCGGACCTGCCGCTGCCGCTGTCGACGCCAGCTTCCTC
HisHisGlnCysProAspProArgThrCysArgCysArgArgSerPheLeu

CGTTGTCAAGGGCGGGCTTAGAGCTCAACCCAGACACACTGCAGGTGCCGGAAGCTGCGA
ArgCysGlnGlyArgGlyLeuGluLeuAsnProAspThrCysArgCysArgLysLeuArg

AGGTGA
ArgEnd

08/469041

```

10      20      30      40      50
MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHH-EVVKFMDVYQRSYCY
: :||: :: : ::::|: : ||:::|| | : |
MRRCRISGRPPAPPGVPAQAPVSQDAPGHQRKVVSIDVYTRATC

```

60 70 80 90 100 110
HPIELTVLDIRQEQYDIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRINKPHI
: : | : : | : | : : : ||| : ||||| : | : ||||| : : : | : : : :
QPREVVPLTVELMGTVAKQLVPSVTVQRCGGCCPDDGLECVPTGQHQVRMOILMIR-Y

```

120      130          140      150      160
QGQHIGEMSFLQHNKCECRPKK-----DRA-----RQEKKSVRGKGKGQKRKRKKSRYY
:: ::|||: : ::|||||| | | | : : |||: : :: : : :
PSSOLGEMSLEEHSOCECRPKKKDSAVKPDRAAATPHHRPOPPRSVPGWDSAPGAPSPADIT

```

170 180 190 200 210
KWSWVPCGPGCSEERRKHLFVQDPQTCKCSCKNTD-SRCKARQLELNERTCRCDKPRR
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OSHSSPRLCPRCTOHOCPDPTCRCRCRRRSFLRCOGRLELNPDTCRCRKLRR

Figure 2. Sequence alignment of VEGF3(lower line) compared to VEGF from human (upper line).

FIGURE 2 1/1